

## SEQUENCE LISTING

<110> BASF Plant Science GmbH

5 <120> Enhanced Amylose Production in Plants

<130> AE884-02

<140> PF0000054331

10 <141> 2003-03-07

<160> 24

<170> PatentIn Ver. 2.1

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<213> Solanum tuberosum

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15	gaa gaa gat gga gct aaa gta gtg aga gta gag aat ctt gag aat cca Glu Glu Asp Gly Ala Lys Val Val Arg Val Glu Asn Leu Glu Asn Pro	115	120	125	384
20	tac aag aaa caa acc aac ttc gac aac aga ttc aag ctt agt cta aac Tyr Lys Lys Gln Thr Asn Phe Asp Asn Arg Phe Lys Leu Ser Leu Asn	130	135	140	432
25	aag ctc tac gct tgg tct ctc tct gat tat gac cgt gtt gta atg ctt Lys Leu Tyr Ala Trp Ser Leu Ser Asp Tyr Asp Arg Val Val Met Leu	145	150	155	480
30	gat gtc gac aat ctc ttt ctc aag aac acc gac gag ctc ttc cag tgt Asp Val Asp Asn Leu Phe Leu Lys Asn Thr Asp Glu Leu Phe Gln Cys	165	170	175	528
35	ggc caa ttt tgt gct gtc ttc atc aac cct tgc atc ttc cac act ggt Gly Gln Phe Cys Ala Val Phe Ile Asn Pro Cys Ile Phe His Thr Gly	180	185	190	576
40	ctc ttt gtg ttg cag cca tca atg gag gtc ttt aga gac atg ctt cat Leu Phe Val Leu Gln Pro Ser Met Glu Val Phe Arg Asp Met Leu His	195	200	205	624
45	gag ctt gaa gta aag aga gat aac cct gat gga gct gat caa ggc ttt Glu Leu Glu Val Lys Arg Asp Asn Pro Asp Gly Ala Asp Gln Gly Phe	210	215	220	672
50	ctt gtc agc tac ttc tct gat tta ctc aat cag cct ctc ttt cgt cct Leu Val Ser Tyr Phe Ser Asp Leu Leu Asn Gln Pro Leu Phe Arg Pro	225	230	235	720
55	cct ccc gat aac cgc acc gcg ctt aag gga cat ttt agg ctt cct ttg Pro Pro Asp Asn Arg Thr Ala Leu Lys Gly His Phe Arg Leu Pro Leu	245	250	255	768
60	gga tat caa atg gac gca tct tat tac tac ctt aag ctc aga tgg aac Gly Tyr Gln Met Asp Ala Ser Tyr Tyr Tyr Leu Lys Leu Arg Trp Asn	260	265	270	816
65	gta cca tgt gga cca aac agt gtg ata acg ttc cca gga gca gta tgg Val Pro Cys Gly Pro Asn Ser Val Ile Thr Phe Pro Gly Ala Val Trp	275	280	285	864
70	tta aag cca tgg tat tgg tgg tca tgg cct gtt ctt cct tta ggc ctt Leu Lys Pro Trp Tyr Trp Trp Ser Trp Pro Val Leu Pro Leu Gly Leu	290	295	300	912
75	tca tgg cac cac caa cgc cgc tac acg att agt tat tca gca gag atg Ser Trp His His Gln Arg Arg Tyr Thr Ile Ser Tyr Ser Ala Glu Met	305	310	315	960
80					

5 cct tgg gtc cta acc caa gca gtg ttc tac cta gga att ata cta gtc 1008  
 Pro Trp Val Leu Thr Gln Ala Val Phe Tyr Leu Gly Ile Ile Leu Val 325 330 335  
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 Thr Arg Leu Ala Arg Pro Asn Met Thr Lys Leu Cys Tyr Arg Arg Ser 340 345 350  
 10 gat aag aat cta agc atg atc cag aca gct ttc aag ttt gtt gca ctc 1104  
 Asp Lys Asn Leu Ser Met Ile Gln Thr Ala Phe Lys Phe Val Ala Leu 355 360 365  
 15 ctc ttt atc ctc tca gcc tac att ata cca ttc ttc atc atc cca cag 1152  
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 20 acg atc cac ccg ctc att ggt tgg tct ctc tac tta acc ggc tcc ttt 1200  
 Thr Ile His Pro Leu Ile Gly Trp Ser Leu Tyr Leu Thr Gly Ser Phe 385 390 395 400  
 25 gct ctc tct acc ata ccc atc aac gcc ttc ttg ctt ccc att ctc cct 1248  
 Ala Leu Ser Thr Ile Pro Ile Asn Ala Phe Leu Leu Pro Ile Leu Pro 405 410 415  
 gtc ata aca ccg tgg ctt ggc att ttc ggg aca ctc ctc gtg atg gct 1296  
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 Phe Pro Ser Tyr Pro Asp Gly Val Val Arg Ala Leu Ser Val Phe Gly 435 440 445  
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 Tyr Ala Phe Cys Cys Ala Pro Phe Leu Trp Val Ser Phe Val Lys Ile 450 455 460  
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 Leu Glu Thr Glu Asn Ala Asn Ala Met Thr Ala Val Met Glu Arg Gly  
 35 40 45  
 60 Leu Lys Thr Gln Arg Arg Pro Glu His Lys Asn Ala Tyr Ala Thr Met  
 50 55 60  
 Met Tyr Met Gly Thr Pro Arg Asp Tyr Glu Phe Tyr Val Ala Thr Arg

## 13

	65					70				75					80	
	Val	Leu	Ile	Arg	Ser	Leu	Lys	Ser	Leu	His	Val	Asp	Ala	Asp	Ile	Val
					85					90					95	
5	Val	Ile	Ala	Ser	Leu	Asp	Val	Pro	Ile	Asn	Trp	Ile	His	Ala	Leu	Glu
				100					105					110		
	Glu	Glu	Asp	Gly	Ala	Lys	Val	Val	Arg	Val	Glu	Asn	Leu	Glu	Asn	Pro
				115					120					125		
	Tyr	Lys	Lys	Gln	Thr	Asn	Phe	Asp	Asn	Arg	Phe	Lys	Leu	Ser	Leu	Asn
							135					140				
10	Lys	Leu	Tyr	Ala	Trp	Ser	Leu	Ser	Asp	Tyr	Asp	Arg	Val	Val	Met	Leu
						150					155				160	
	Asp	Val	Asp	Asn	Leu	Phe	Leu	Lys	Asn	Thr	Asp	Glu	Leu	Phe	Gln	Cys
					165					170					175	
15	Gly	Gln	Phe	Cys	Ala	Val	Phe	Ile	Asn	Pro	Cys	Ile	Phe	His	Thr	Gly
				180					185					190		
	Leu	Phe	Val	Leu	Gln	Pro	Ser	Met	Glu	Val	Phe	Arg	Asp	Met	Leu	His
				195				200					205			
	Glu	Leu	Glu	Val	Lys	Arg	Asp	Asn	Pro	Asp	Gly	Ala	Asp	Gln	Gly	Phe
				210			215					220				
20	Leu	Val	Ser	Tyr	Phe	Ser	Asp	Leu	Leu	Asn	Gln	Pro	Leu	Phe	Arg	Pro
						230					235				240	
	Pro	Pro	Asp	Asn	Arg	Thr	Ala	Leu	Lys	Gly	His	Phe	Arg	Leu	Pro	Leu
					245					250					255	
25	Gly	Tyr	Gln	Met	Asp	Ala	Ser	Tyr	Tyr	Tyr	Leu	Lys	Leu	Arg	Trp	Asn
				260					265					270		
	Val	Pro	Cys	Gly	Pro	Asn	Ser	Val	Ile	Thr	Phe	Pro	Gly	Ala	Val	Trp
				275				280					285			
	Leu	Lys	Pro	Trp	Tyr	Trp	Trp	Ser	Trp	Pro	Val	Leu	Pro	Leu	Gly	Leu
						295					300					
30	Ser	Trp	His	His	Gln	Arg	Tyr	Thr	Ile	Ser	Tyr	Ser	Ala	Glu	Met	
						310				315					320	
	Pro	Trp	Val	Leu	Thr	Gln	Ala	Val	Phe	Tyr	Leu	Gly	Ile	Ile	Leu	Val
					325					330					335	
35	Thr	Arg	Leu	Ala	Arg	Pro	Asn	Met	Thr	Lys	Leu	Cys	Tyr	Arg	Arg	Ser
				340					345					350		
	Asp	Lys	Asn	Leu	Ser	Met	Ile	Gln	Thr	Ala	Phe	Lys	Phe	Val	Ala	Leu
				355				360					365			
	Leu	Phe	Ile	Leu	Ser	Ala	Tyr	Ile	Ile	Pro	Phe	Phe	Ile	Ile	Pro	Gln
							375				380					
40	Thr	Ile	His	Pro	Leu	Ile	Gly	Trp	Ser	Leu	Tyr	Leu	Thr	Gly	Ser	Phe
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## 14

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1494)

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Met	Asp	Leu	Gln	Arg	Gly	Phe	Val	Phe	Leu	Ser	Leu	Val	Leu	Ser	Phe	
1				5					10					15		

10	atg	ata	atc	gaa	acg	acg	gcg	tat	cga	gag	aga	cag	ctg	ctg	ctg	ctg	96
	Met	Ile	Ile	Glu	Thr	Thr	Ala	Tyr	Arg	Glu	Arg	Gln	Leu	Leu	Leu	Leu	
			20						25					30			

15	caa	cca	ccg	caa	gaa	acg	gcg	ata	gat	acc	gca	aac	gcg	gtg	gtg	acg	144
	Gln	Pro	Pro	Gln	Glu	Thr	Ala	Ile	Asp	Thr	Ala	Asn	Ala	Val	Val	Thr	
			35					40					45				

20	gtt	caa	gat	cga	ggg	ttg	aag	acg	cgg	cga	ccg	gag	cat	aag	aac	gca	192
	Val	Gln	Asp	Arg	Gly	Leu	Lys	Thr	Arg	Arg	Pro	Glu	His	Lys	Asn	Ala	
		50					55					60					

25	tac	gca	acg	atg	atg	tac	atg	ggg	acg	cca	aga	gac	tac	gag	ttc	tac	240
	Tyr	Ala	Thr	Met	Met	Tyr	Met	Gly	Thr	Pro	Arg	Asp	Tyr	Glu	Phe	Tyr	
		65				70					75					80	

	gtt	gcg	aca	cgt	gtt	ttg	atc	aga	tcg	ttg	aga	agt	ctt	cac	gtg	gaa	288
	Val	Ala	Thr	Arg	Val	Leu	Ile	Arg	Ser	Leu	Arg	Ser	Leu	His	Val	Glu	
				85						90					95		

30	gct	gat	ctc	gtc	gtc	atc	gct	tct	ctc	gac	gtt	cct	ctc	cga	tgg	gtt	336
	Ala	Asp	Leu	Val	Val	Ile	Ala	Ser	Leu	Asp	Val	Pro	Leu	Arg	Trp	Val	
				100					105					110			

35	caa	acc	ttg	gaa	gag	gaa	gat	gga	gct	aaa	gtg	gtg	aga	gtt	gaa	aat	384
	Gln	Thr	Leu	Glu	Glu	Glu	Asp	Gly	Ala	Lys	Val	Val	Arg	Val	Glu	Asn	
			115					120					125				

40	gtg	gat	aat	cca	tac	agg	aga	cag	acc	aac	ttc	aac	agt	aga	ttc	aag	432
	Val	Asp	Asn	Pro	Tyr	Arg	Arg	Gln	Thr	Asn	Phe	Asn	Ser	Arg	Phe	Lys	
		130					135					140					

45	ctt	act	cta	aac	aag	ctc	tac	gct	tgg	gct	ttg	tct	gat	tac	gac	cgt	480
	Leu	Thr	Leu	Asn	Lys	Leu	Tyr	Ala	Trp	Ala	Leu	Ser	Asp	Tyr	Asp	Arg	
		145				150					155					160	

	gtg	gtc	atg	cta	gat	gcc	gat	aac	ctc	ttt	ctt	aag	aaa	gcc	gac	gag	528
	Val	Val	Met	Leu	Asp	Ala	Asp	Asn	Leu	Phe	Leu	Lys	Lys	Ala	Asp	Glu	
					165					170					175		

50	ttg	ttc	cag	tgt	ggg	cgc	ttc	tgt	gcg	gtc	ttc	att	aac	cct	tgt	atc	576
	Leu	Phe	Gln	Cys	Gly	Arg	Phe	Cys	Ala	Val	Phe	Ile	Asn	Pro	Cys	Ile	
				180					185					190			

55	ttc	cac	act	ggg	ctc	ttc	gtg	ttg	cag	cca	tca	gtg	gaa	gtg	ttc	aag	624
	Phe	His	Thr	Gly	Leu	Phe	Val	Leu	Gln	Pro	Ser	Val	Glu	Val	Phe	Lys	
			195					200					205				

60	gac	atg	ctc	cat	gag	cta	caa	gtt	gga	aga	aag	aat	cct	gat	gga	gct	672
	Asp	Met	Leu	His	Glu	Leu	Gln	Val	Gly	Arg	Lys	Asn	Pro	Asp	Gly	Ala	
		210					215					220					

## 15

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5	ctc ttt agt cct ccg agt aac gga tct gta ctt aat ggt cac ttg aga	768
	Leu Phe Ser Pro Pro Ser Asn Gly Ser Val Leu Asn Gly His Leu Arg	
	245 250 255	
10	ctt ccc tta ggc tac caa atg gac gct tct tat ttc tat ctt aag cta	816
	Leu Pro Leu Gly Tyr Gln Met Asp Ala Ser Tyr Phe Tyr Leu Lys Leu	
	260 265 270	
15	aga tgg aac ata ccc tgt gga cca aac agt gtg att aca ttc ccg gga	864
	Arg Trp Asn Ile Pro Cys Gly Pro Asn Ser Val Ile Thr Phe Pro Gly	
	275 280 285	
20	gct gtt tgg tta aag cca tgg tac tgg tgg tca tgg cct gtt ctt cca	912
	Ala Val Trp Leu Lys Pro Trp Tyr Trp Trp Ser Trp Pro Val Leu Pro	
	290 295 300	
	cta ggt ttc tca tgg cac gag cag cgt cgc gcc act ata ggg tac tca	960
	Leu Gly Phe Ser Trp His Glu Gln Arg Arg Ala Thr Ile Gly Tyr Ser	
	305 310 315 320	
25	gcc gaa atg cct ttg gtt ata atc caa gca atg ttt tac ctt gga atc	1008
	Ala Glu Met Pro Leu Val Ile Ile Gln Ala Met Phe Tyr Leu Gly Ile	
	325 330 335	
30	ata gtg gtt aca cga cta gct cgt cct aac ata acc aag cta tgt tat	1056
	Ile Val Val Thr Arg Leu Ala Arg Pro Asn Ile Thr Lys Leu Cys Tyr	
	340 345 350	
35	cgc cgc tct gac cgc aac tta aca acg atc caa gct ggt ttt aag ttg	1104
	Arg Arg Ser Asp Arg Asn Leu Thr Thr Ile Gln Ala Gly Phe Lys Leu	
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40	atc gcg ctt ctc tct gta gtt gca gcc tac atc ttc cca ttc ttc acc	1152
	Ile Ala Leu Leu Ser Val Val Ala Ala Tyr Ile Phe Pro Phe Phe Thr	
	370 375 380	
	atc cct cac act atc cac cca ctc atc ggc tgg tcg ctc tac ttg atg	1200
	Ile Pro His Thr Ile His Pro Leu Ile Gly Trp Ser Leu Tyr Leu Met	
	385 390 395 400	
45	gct tct ttt gct ctc tct tcc att tca atc aac act ctc ctc ctc cca	1248
	Ala Ser Phe Ala Leu Ser Ser Ile Ser Ile Asn Thr Leu Leu Leu Pro	
	405 410 415	
50	acg ctc cct gtt ctc act cca tgg cta gga att ctc ggc act ctc ctt	1296
	Thr Leu Pro Val Leu Thr Pro Trp Leu Gly Ile Leu Gly Thr Leu Leu	
	420 425 430	
55	gtc atg gcc ttc cct tgg tac cct gat gga gtg gtc aga gcc ttg tca	1344
	Val Met Ala Phe Pro Trp Tyr Pro Asp Gly Val Val Arg Ala Leu Ser	
	435 440 445	
60	gtt ttc gca tac gca ttt tgt tgc gca ccc ttt gtg tgg gtt tca ttc	1392
	Val Phe Ala Tyr Ala Phe Cys Cys Ala Pro Phe Val Trp Val Ser Phe	
	450 455 460	
	cgc aaa atc aca tcg cac ctc cag gtt ttg att gag aaa gag gtg ttg	1440

## 16

Arg Lys Ile Thr Ser His Leu Gln Val Leu Ile Glu Lys Glu Val Leu  
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5 ttc ccg cga ttg gga gac tca ggg gtc act tca ggc ttc agc aaa ttg 1488  
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25 Val Gln Asp Arg Gly Leu Lys Thr Arg Arg Pro Glu His Lys Asn Ala  
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 Tyr Ala Thr Met Met Tyr Met Gly Thr Pro Arg Asp Tyr Glu Phe Tyr  
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35 Val Asp Asn Pro Tyr Arg Arg Gln Thr Asn Phe Asn Ser Arg Phe Lys  
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40 Leu Phe Gln Cys Gly Arg Phe Cys Ala Val Phe Ile Asn Pro Cys Ile  
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45 Asp Met Leu His Glu Leu Gln Val Gly Arg Lys Asn Pro Asp Gly Ala  
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 275 280 285

55 Ala Val Trp Leu Lys Pro Trp Tyr Trp Trp Ser Trp Pro Val Leu Pro  
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 305 310 315 320  
 Ala Glu Met Pro Leu Val Ile Ile Gln Ala Met Phe Tyr Leu Gly Ile  
 325 330 335

60 Ile Val Val Thr Arg Leu Ala Arg Pro Asn Ile Thr Lys Leu Cys Tyr  
 340 345 350



## 17

Arg Arg Ser Asp Arg Asn Leu Thr Thr Ile Gln Ala Gly Phe Lys Leu  
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 5 Ile Pro His Thr Ile His Pro Leu Ile Gly Trp Ser Leu Tyr Leu Met  
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 420 425 430  
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 435 440 445  
 Val Phe Ala Tyr Ala Phe Cys Cys Ala Pro Phe Val Trp Val Ser Phe  
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 15 Arg Lys Ile Thr Ser His Leu Gln Val Leu Ile Glu Lys Glu Val Leu  
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 20 25 30  
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 Ser Ser Gln Ser Ser His Arg Leu Tyr Ile Ser Ser Glu Lys Thr Lys  
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 Thr Lys Arg Phe Gln Arg Asn Gly Tyr Thr Leu Asp Val Glu Met Cys  
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 Val Asn Phe Ser Ser Leu Lys Leu Val Leu Phe Leu Met Met Leu Val  
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 85 90 95  
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 Pro Ser Ser Phe Ala Asn Lys Trp Ile Leu Glu Pro Ala Val Thr Thr  
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 60 gat cct cgc tat ata gct aca tct gag atc aac tgg aac agt atg tca 384

## 18

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	Leu	Val	Val	Glu	His	Tyr	Leu	Ser	Gly	Arg	Ser	Glu	Tyr	Gln	Gly	Ile	
		130					135					140					
10	ggc	ttt	cta	aat	ctc	aac	gat	aac	gag	att	aat	cga	tgg	cag	gtg	gtc	480
	Gly	Phe	Leu	Asn	Leu	Asn	Asp	Asn	Glu	Ile	Asn	Arg	Trp	Gln	Val	Val	
	145					150					155					160	
15	ata	aaa	tct	cac	tgt	cag	cat	ata	gct	ttg	cat	cta	gac	cat	gct	gca	528
	Ile	Lys	Ser	His	Cys	Gln	His	Ile	Ala	Leu	His	Leu	Asp	His	Ala	Ala	
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	Ser	Asn	Ile	Thr	Trp	Lys	Ser	Leu	Tyr	Pro	Glu	Trp	Ile	Asp	Glu	Glu	
				180					185					190			
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	Pro	Asp	Lys	Ser	Arg	Ile	Asp	Leu	Ile	Ile	Ala	Lys	Leu	Pro	Cys	Asn	
		210					215					220					
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	Lys	Ser	Gly	Lys	Trp	Ser	Arg	Asp	Val	Ala	Arg	Leu	His	Leu	Gln	Leu	
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	Val	Ile	Leu	Val	Ser	Asp	Cys	Phe	Pro	Ile	Pro	Asn	Leu	Phe	Thr	Gly	
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	Leu	His	Gln	Leu	Arg	Gln	Lys	Leu	Gln	Leu	Pro	Val	Gly	Ser	Cys	Glu	
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Glu Lys Phe Lys Val Pro Thr Cys Pro Ser Leu Pro Trp Ile Gln Val  
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Lys Ser Gly Lys Trp Ser Arg Asp Val Ala Arg Leu His Leu Gln Leu  
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Gln Glu Leu Val Ala Arg Gln Gly Asn Ile Trp Leu Tyr Lys Pro Lys  
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## 21

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				Cys	Leu	Leu	Ser	Ser	Lys	Gln	Lys	Ala	Gln	Leu	Glu	Trp	Asp	Arg	Arg
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							610			615				620					
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	Val Lys Phe Asn Thr Leu Lys Leu Val Leu Ile Cys Ile Met Leu Gly	
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10	gct ttg ttc acg atc tac cgt ttt cgt tat cca ccg cta caa att cct	192
	Ala Leu Phe Thr Ile Tyr Arg Phe Arg Tyr Pro Pro Leu Gln Ile Pro	
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15	gaa att cca act agt ttt ggt ctt act act gat cct cgc tat gta gct	240
	Glu Ile Pro Thr Ser Phe Gly Leu Thr Thr Asp Pro Arg Tyr Val Ala	
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20	aca gct gag atc aac tgg aac cat atg tca aat ctt gtt gag aag cac	288
	Thr Ala Glu Ile Asn Trp Asn His Met Ser Asn Leu Val Glu Lys His	
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	Asp Asn Glu Ile Asp Arg Phe Lys Glu Val Thr Lys Ser Asp Cys Asp	
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	165 170 175	
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	Asp Leu Val Ile Ala Lys Leu Pro Cys Asp Lys Ser Gly Lys Trp Ser	
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	Arg Asp Val Ala Arg Leu His Leu Gln Leu Ala Ala Arg Val Ala	
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	Cys Phe Pro Ile Pro Asn Leu Phe Thr Gly Gln Glu Leu Val Ala Arg	
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	Gln Gly Asn Ile Trp Leu Tyr Lys Pro Asn Leu His Gln Leu Arg Gln	
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75	aag tta cag ctt cct gtt ggt tcc tgt gaa ctt tct gtt cct ctt caa	816
	Lys Leu Gln Leu Pro Val Gly Ser Cys Glu Leu Ser Val Pro Leu Gln	
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	Ala Gln Ser Ile Arg Met Ser Gly Ser Thr Arg Asp Leu Val Ile Leu	
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	Val Asp Glu Thr Ile Ser Glu Tyr His Lys Ser Gly Leu Val Ala Ala	
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	Leu Thr Glu Tyr Ser Lys Ile Ile Phe Ile Asp Ala Asp Met Leu Ile	
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40	tct aat tca aca ttc cag tta cta atg gat aac att aat gaa gtt gtg	1296
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	His	Val	Ala	Leu	His	Leu	Asp	Tyr	Ala	Ala	Lys	Asn	Ile	Thr	Trp	Glu	
	130						135					140					
	Ser	Leu	Tyr	Pro	Glu	Trp	Ile	Asp	Glu	Val	Glu	Phe	Glu	Val	Pro		
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15	aga ttc cgg aga aat agc aaa gga ggt ggc aga tcg gat atg gtg aaa	144
	Arg Phe Arg Arg Asn Ser Lys Gly Gly Gly Arg Ser Asp Met Val Lys	
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	Pro Phe Asn Ile Ile Asn Phe Ser Thr Gln Asp Lys Asn Ser Ser Cys	
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	Cys Cys Phe Thr Lys Phe Gln Ile Val Lys Leu Leu Leu Phe Ile Leu	
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30	ctc tct gcc act ctc ttc acc att atc tat tct cct gaa gct tat cat	288
	Leu Ser Ala Thr Leu Phe Thr Ile Ile Tyr Ser Pro Glu Ala Tyr His	
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35	cat tct ctt tcc cac tca tct tct cga tgg ata tgg aga aga caa gat	336
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	Pro Arg Tyr Phe Ser Asp Leu Asp Ile Asn Trp Asp Asp Val Thr Lys	
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	Pro Thr Arg Arg Leu Asp Leu Ile Val Val Lys Leu Pro Cys Arg Lys	
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## 27

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20	gat acc ttg aga gac aag ctt cag ctg cct gta ggg tct tgt gag cta Asp Thr Leu Arg Asp Lys Leu Gln Leu Pro Val Gly Ser Cys Glu Leu	290	295	300	912
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35	ggt gca atc gcc gcg gct cag agc ata aga cag tct ggt tcg acg aga Gly Ala Ile Ala Ala Ala Gln Ser Ile Arg Gln Ser Gly Ser Thr Arg	340	345	350	1056
40	gac ctt gtt atc ctt gtt gat gac aac atc agc ggt tac cac cgg agt Asp Leu Val Ile Leu Val Asp Asp Asn Ile Ser Gly Tyr His Arg Ser	355	360	365	1104
45	gga cta gaa gcc gcg ggt tgg caa atc cgg acg ata cag agg att cga Gly Leu Glu Ala Ala Gly Trp Gln Ile Arg Thr Ile Gln Arg Ile Arg	370	375	380	1152
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55	ttc cgg cta tgg cag ctg act gat tac gac aaa atc att ttc atc gac Phe Arg Leu Trp Gln Leu Thr Asp Tyr Asp Lys Ile Ile Phe Ile Asp	405	410	415	1248
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75	ata aac gag att gag tct tat aac ggt gga gat caa ggt tac tta aac Ile Asn Glu Ile Glu Ser Tyr Asn Gly Gly Asp Gln Gly Tyr Leu Asn	465	470	475	1440
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40	gat	att	caa	caa	cag	ctt	gcg	att	cct	aat	tgg	gaa	cag	gct	atg	aga	816
	Asp	Ile	Gln	Gln	Gln	Leu	Ala	Ile	Pro	Asn	Trp	Glu	Gln	Ala	Met	Arg	
				260					265					270			
45	tta	cct	ggt	tat	atg	tct	agg	atg	cct	aaa	cct	ccg	gaa	gat	tct	cat	864
	Leu	Pro	Gly	Tyr	Met	Ser	Arg	Met	Pro	Lys	Pro	Pro	Glu	Asp	Ser	His	
			275					280					285				
50	ttg	gag	cag	att	gtt	agg	ttg	att	tct	gag	tct	aag	aag	cct	gtg	ttg	912
	Leu	Glu	Gln	Ile	Val	Arg	Leu	Ile	Ser	Glu	Ser	Lys	Lys	Pro	Val	Leu	
		290					295					300					
55	tat	gtt	ggt	ggt	ggt	tgt	ttg	aac	tct	agc	gat	gaa	ttg	ggt	agg	ttt	960
	Tyr	Val	Gly	Gly	Gly	Cys	Leu	Asn	Ser	Ser	Asp	Glu	Leu	Gly	Arg	Phe	
	305					310					315					320	
60	gtt	gag	ctt	acg	gga	atc	cct	gtt	gcg	agt	acg	ttg	atg	ggg	ctg	gga	1008
	Val	Glu	Leu	Thr	Gly	Ile	Pro	Val	Ala	Ser	Thr	Leu	Met	Gly	Leu	Gly	
				325						330					335		
65	tct	tat	cct	tgt	gat	gat	gag	ttg	tcg	tta	cat	atg	ctt	gga	atg	cat	1056
	Ser	Tyr	Pro	Cys	Asp	Asp	Glu	Leu	Ser	Leu	His	Met	Leu	Gly	Met	His	
				340					345					350			
70	ggg	act	gtg	tat	gca	aat	tac	gct	gtg	gag	cat	agt	gat	ttg	ttg	ttg	1104
	Gly	Thr	Val	Tyr	Ala	Asn	Tyr	Ala	Val	Glu	His	Ser	Asp	Leu	Leu	Leu	
			355					360					365				
75	gcg	ttt	ggg	gta	agg	ttt	gat	gat	cgt	gtc	acg	ggt	aaa	ctt	gag	gct	1152
	Ala	Phe	Gly	Val	Arg	Phe	Asp	Asp	Arg	Val	Thr	Gly	Lys	Leu	Glu	Ala	

	370	375	380	
5	ttt gct agt agg gct aag att gtt cat att gat att gac tcg gct gag Phe Ala Ser Arg Ala Lys Ile Val His Ile Asp Ile Asp Ser Ala Glu 385 390 395 400	1200		
10	att ggg aag aat aag act cct cat gtg tct gtg tgt ggt gat gtt aag Ile Gly Lys Asn Lys Thr Pro His Val Ser Val Cys Gly Asp Val Lys 405 410 415	1248		
15	ctg gct ttg caa ggg atg aat aag gtt ctt gag aac cga gcg gag gag Leu Ala Leu Gln Gly Met Asn Lys Val Leu Glu Asn Arg Ala Glu Glu 420 425 430	1296		
20	ctt aaa ctt gat ttt gga gtt tgg agg aat gag ttg aac gta cag aaa Leu Lys Leu Asp Phe Gly Val Trp Arg Asn Glu Leu Asn Val Gln Lys 435 440 445	1344		
25	cag aag ttt ccg ttg agc ttt aag acg ttt ggg gaa gct att cct cca Gln Lys Phe Pro Leu Ser Phe Lys Thr Phe Gly Glu Ala Ile Pro Pro 450 455 460	1392		
30	cag tat gcg att aag gtc ctt gat gag ttg act gat gga aaa gcc ata Gln Tyr Ala Ile Lys Val Leu Asp Glu Leu Thr Asp Gly Lys Ala Ile 465 470 475 480	1440		
35	ata agt act ggt gtc ggg caa cat caa atg tgg gcg gcg cag ttc tac Ile Ser Thr Gly Val Gly Gln His Gln Met Trp Ala Ala Gln Phe Tyr 485 490 495	1488		
40	aat tac aag aaa cca agg cag tgg cta tca tca gga ggc ctt gga gct Asn Tyr Lys Lys Pro Arg Gln Trp Leu Ser Ser Gly Gly Leu Gly Ala 500 505 510	1536		
45	atg gga ttt gga ctt cct gct gcg att gga gcg tct gtt gct aac cct Met Gly Phe Gly Leu Pro Ala Ala Ile Gly Ala Ser Val Ala Asn Pro 515 520 525	1584		
50	gat gcg ata gtt gtg gat att gac gga gat gga agt ttt ata atg aat Asp Ala Ile Val Val Asp Ile Asp Gly Asp Gly Ser Phe Ile Met Asn 530 535 540	1632		
55	gtg caa gag cta gcc act att cgt gta gag aat ctt cca gtg aag gta Val Gln Glu Leu Ala Thr Ile Arg Val Glu Asn Leu Pro Val Lys Val 545 550 555 560	1680		
60	ctt tta tta aac aac cag cat ctt ggc atg gtt atg caa tgg gaa gat Leu Leu Leu Asn Asn Gln His Leu Gly Met Val Met Gln Trp Glu Asp 565 570 575	1728		
65	cgg ttc tac aaa gct aac cga gca cac aca ttt ctc gga gat ccg gct Arg Phe Tyr Lys Ala Asn Arg Ala His Thr Phe Leu Gly Asp Pro Ala 580 585 590	1776		
70	cag gag gac gag ata ttc ccg aac atg ttg ctg ttt gca gca gct tgc Gln Glu Asp Glu Ile Phe Pro Asn Met Leu Leu Phe Ala Ala Ala Cys 595 600 605	1824		
75	ggg att cca gcg gcg agg gtg aca aag aaa gca gat ctc cga gaa gct Gly Ile Pro Ala Ala Arg Val Thr Lys Lys Ala Asp Leu Arg Glu Ala 610 615 620	1872		

att cag aca atg ctg gat aca cca gga cct tac ctg ttg gat gtg att 1920  
 Ile Gln Thr Met Leu Asp Thr Pro Gly Pro Tyr Leu Leu Asp Val Ile  
 625 630 635 640

5 tgt ccg cac caa gaa cat gtg ttg ccg atg atc ccg aat ggt ggc act 1968  
 Cys Pro His Gln Glu His Val Leu Pro Met Ile Pro Asn Gly Gly Thr  
 645 650 655

10 ttc aac gat gtc ata acg gaa gga gat ggc cgg att aaa tac tgagagctc 2019  
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Arg Phe Ser Leu Pro Phe Ser Leu Asn Pro Asn Lys Ser Ser Ser Ser  
 35 40 45

30 Ser Arg Arg Arg Gly Ile Lys Ser Ser Ser Pro Ser Ser Ile Ser Ala  
 50 55 60

35 Val Leu Asn Thr Thr Thr Asn Val Thr Thr Thr Pro Ser Pro Thr Lys  
 65 70 75 80

Pro Thr Lys Pro Glu Thr Phe Ile Ser Arg Phe Ala Pro Asp Gln Pro  
 85 90 95

40 Arg Lys Gly Ala Asp Ile Leu Val Glu Ala Leu Glu Arg Gln Gly Val  
 100 105 110

Glu Thr Val Phe Ala Tyr Pro Gly Gly Ala Ser Met Glu Ile His Gln  
 115 120 125

45 Ala Leu Thr Arg Ser Ser Ser Ile Arg Asn Val Leu Pro Arg His Glu  
 130 135 140

50 Gln Gly Gly Val Phe Ala Ala Glu Gly Tyr Ala Arg Ser Ser Gly Lys  
 145 150 155 160

Pro Gly Ile Cys Ile Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val  
 165 170 175

55 Ser Gly Leu Ala Asp Ala Leu Leu Asp Ser Val Pro Leu Val Ala Ile  
 180 185 190

Thr Gly Gln Val Pro Arg Arg Met Ile Gly Thr Asp Ala Phe Gln Glu  
 195 200 205

60 Thr Pro Ile Val Glu Val Thr Arg Ser Ile Thr Lys His Asn Tyr Leu  
 210 215 220

Val Met Asp Val Glu Asp Ile Pro Arg Ile Ile Glu Glu Ala Phe Phe  
 225 230 235 240  
 5 Leu Ala Thr Ser Gly Arg Pro Gly Pro Val Leu Val Asp Val Pro Lys  
 245 250 255  
 Asp Ile Gln Gln Gln Leu Ala Ile Pro Asn Trp Glu Gln Ala Met Arg  
 260 265 270  
 10 Leu Pro Gly Tyr Met Ser Arg Met Pro Lys Pro Pro Glu Asp Ser His  
 275 280 285  
 Leu Glu Gln Ile Val Arg Leu Ile Ser Glu Ser Lys Lys Pro Val Leu  
 290 295 300  
 Tyr Val Gly Gly Gly Cys Leu Asn Ser Ser Asp Glu Leu Gly Arg Phe  
 305 310 315 320  
 20 Val Glu Leu Thr Gly Ile Pro Val Ala Ser Thr Leu Met Gly Leu Gly  
 325 330 335  
 Ser Tyr Pro Cys Asp Asp Glu Leu Ser Leu His Met Leu Gly Met His  
 340 345 350  
 25 Gly Thr Val Tyr Ala Asn Tyr Ala Val Glu His Ser Asp Leu Leu Leu  
 355 360 365  
 Ala Phe Gly Val Arg Phe Asp Asp Arg Val Thr Gly Lys Leu Glu Ala  
 370 375 380  
 Phe Ala Ser Arg Ala Lys Ile Val His Ile Asp Ile Asp Ser Ala Glu  
 385 390 395 400  
 35 Ile Gly Lys Asn Lys Thr Pro His Val Ser Val Cys Gly Asp Val Lys  
 405 410 415  
 Leu Ala Leu Gln Gly Met Asn Lys Val Leu Glu Asn Arg Ala Glu Glu  
 420 425 430  
 40 Leu Lys Leu Asp Phe Gly Val Trp Arg Asn Glu Leu Asn Val Gln Lys  
 435 440 445  
 Gln Lys Phe Pro Leu Ser Phe Lys Thr Phe Gly Glu Ala Ile Pro Pro  
 450 455 460  
 Gln Tyr Ala Ile Lys Val Leu Asp Glu Leu Thr Asp Gly Lys Ala Ile  
 465 470 475 480  
 50 Ile Ser Thr Gly Val Gly Gln His Gln Met Trp Ala Ala Gln Phe Tyr  
 485 490 495  
 Asn Tyr Lys Lys Pro Arg Gln Trp Leu Ser Ser Gly Gly Leu Gly Ala  
 500 505 510  
 55 Met Gly Phe Gly Leu Pro Ala Ala Ile Gly Ala Ser Val Ala Asn Pro  
 515 520 525  
 Asp Ala Ile Val Val Asp Ile Asp Gly Asp Gly Ser Phe Ile Met Asn  
 530 535 540  
 60



## 41

Val Gln Glu Leu Ala Thr Ile Arg Val Glu Asn Leu Pro Val Lys Val  
 545 550 555 560

5 Leu Leu Leu Asn Asn Gln His Leu Gly Met Val Met Gln Trp Glu Asp  
 565 570 575

Arg Phe Tyr Lys Ala Asn Arg Ala His Thr Phe Leu Gly Asp Pro Ala  
 580 585 590

10 Gln Glu Asp Glu Ile Phe Pro Asn Met Leu Leu Phe Ala Ala Ala Cys  
 595 600 605

Gly Ile Pro Ala Ala Arg Val Thr Lys Lys Ala Asp Leu Arg Glu Ala  
 610 615 620

15 Ile Gln Thr Met Leu Asp Thr Pro Gly Pro Tyr Leu Leu Asp Val Ile  
 625 630 635 640

20 Cys Pro His Gln Glu His Val Leu Pro Met Ile Pro Asn Gly Gly Thr  
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Phe Asn Asp Val Ile Thr Glu Gly Asp Gly Arg Ile Lys Tyr  
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25

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 <222> (1)..(259)  
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 tatattaatg ttttaaatc ctttatagtg ataaagatgg ttcgaaacat gctacaaatt 180  
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 45 tagataccag cccgggccc 259

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 50 <212> DNA  
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<220>  
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<220>

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 ggatgtggga ttcccgcctc ttttaactatg gaaactggga ggtacttagg tatcttctct 180

caaatgcgag atggttggttg ccatttcaca tcaccagaag gaatacctgg agttccagaa 240  
 acaaatttca atggtcgctcc aaattccttc aaagtgtgtg ctctgctgcg aacatgtgtg 300  
 gcttattaca gagttgacga acgcatgtca gaaactgaag tttaccagac agacatttct 360  
 agtgagctac taccaacagc caatatcgag gagagtgcg 400

5

&lt;210&gt; 20

&lt;211&gt; 1105

&lt;212&gt; DNA

10 &lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:RNAifragment

15 &lt;220&gt;

&lt;400&gt; 20

gaattgttgt tctcatggac atcgttcaca gccatgcac aaataatact ttagatggac 60  
 tgaacatgtt tgacggcacc gatagttgtt actttcactc tggagctcgt ggttatcatt 120  
 ggatgtggga ttcccgctc tttaactatg gaaactggga ggtacttagg tatcttctct 180  
 caaatgcgag atggttggttg ccatttcaca tcaccagaag gaatacctgg agttccagaa 240  
 acaaatttca atggtcgctcc aaattccttc aaagtgtgtg ctctgctgcg aacatgtgtg 300  
 gcttattaca gagttgacga acgcatgtca gaaactgaag tttaccagac agacatttct 360  
 agtgagctac taccaacagc caatatcgag gagagtgcg atcaagctga tctctaaata 420  
 attcgaaata tctttgttat tatttttttc tattcaaatt gcaattagac ataagtcatt 480  
 ttaactgaag ttgcattgat gaaaaattat actatgtttt atgtatatat attaatTTTT 540  
 aaattccttt atagtataaa agatagttcg aaacatgcta taaattatta tacgaattta 600  
 cgttactttt tttaatctac tttaacaatt ttctaatttc actattgaac atagatacca 660  
 gcccgggccg tcgacctcga attcgccctt ggagagtgcg gttcgcgtca ctctcctcga 720  
 tattggctgt tggtagtagc tctactagaa tgtctgtctg gtaaaacttca gtttctgaca 780  
 tgcgttcgtc aactctgtaa taagccacac atgttcgcgc aggagacagc actttgaagg 840  
 aatttgagc accattgaaa tttgtttctg gaactccagg tattccttct ggtgatgtga 900  
 aatggcaacc accatctcgc atttgagaga agatacctaa gtacctccca gtttccatag 960  
 ttaaagagc gggaaatcca catccaatga taaccacgag ctccagagtg aaagtaacaa 1020  
 ctatcggtgc cgtcaaacat gttcagtcga tctaaagtat tatttgatgc atggctgtga 1080  
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40 &lt;210&gt; 21

&lt;211&gt; 180

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

45 &lt;223&gt; Description of Artificial Sequence:SBE RNAi 1

&lt;220&gt;

&lt;400&gt; 21

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 aacagccaat atcgaggaga gtgacgttcg cgtcactctc ctcgatattg gctgttggtg 120  
 gtagctcact caaccacat ctgcatttg agagaagata cctaagtacc ttttgggtacc 180

55 &lt;210&gt; 22

&lt;211&gt; 420

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

60 &lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:SBE RNAi 2

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 5 ctgggaggta cttaggtatc ttctctcaaa tgcgagatgg tggttggctt attacagagt 120  
 tgacgaacgc atgtcagaaa ctgaagttta ccagacagac atttctagtg agctactacc 180  
 aacagccaat atcgaggaga gtgacgttcg cgtcactctc ctcgatattg gctggttgta 240  
 gtagctcact agaaatgtct gtctggtaaa cttcagtttc tgacatgcgt tcgtcaactc 300  
 tgtaataagc caaccacat ctgcatttg agagaagata cctaagtacc tcccagtttc 360  
 10 catagttaaa gaggcgggaa tcccacatcc aatgataacc acgagctcca ttttgggtacc 420

<210> 23  
 <211> 37  
 <212> DNA  
 15 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence:spacer

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 <400> 23  
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25 <210> 24  
 <211> 837  
 <212> DNA  
 <213> Artificial Sequence  
 30 <220>  
 <223> Description of Artificial Sequence:fragment of be2  
 and bel in pHAS3 for RNAi

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 40 tgaacatgtt tgacggcacc gatagttgtt actttcactc tggagctcgt gggttatcatt 120  
 ggatgtggga ttcccgccctc ttttaactatg gaaactggga ggtacttagg tatcttctct 180  
 caaatgagag atggtgggtg ccatttcaca tcaccagaag gaataacctg agttccagaa 240  
 acaaatttca atggtcgctc aaattccttc aaagtgtgt ctctgctgag aacatgtgtg 300  
 gcttattaca gagttgacga acgcatgtca gaaactgaag tttaccagac agacatttct 360  
 45 agtgagctac taccaacagc caatatcgag gagagtgcg atcaagctta tcgataccgt 420  
 cgacctcgaa gcttgatcgt cactctctc gatattggct gttggtagta gctcactaga 480  
 aatgtctgtc tggtaaactt cagtttctga catgcgttcg tcaactctgt aataagccac 540  
 acatgttcgc gcaggagaca gcactttgaa ggaatttgga cgaccattga aatttgtttc 600  
 tggaactcca ggtattcctt ctggtgatgt gaaatggcaa ccaccatctc gcatttgaga 660  
 50 gaagatacct aagtacctc cagtttccat agttaagag gcgggaatcc cacatccaat 720  
 gataaccacg agtccagag tgaaagtaac aactatcggt gccgtcaaac atgttcagtc 780  
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